

F/G. 1

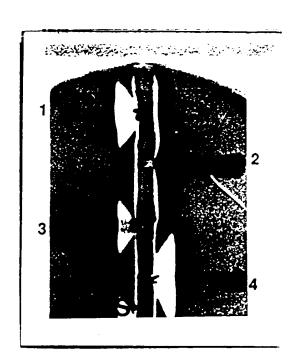


FIG. 3B

FIG. 3A

AAT	caaaataaaaattaatatatattttatgataatcacatatat <u>ttgac</u> -35	09
	+1 ATTGTTACTG <u>TATGA</u> TACAGGCATAAGTACTTATTTTATTAGATTGCAA -10	120
	SAATTATATTTTCA <u>AAGAGG</u> AATGCTT ATG GAA TTC AAA AAG TTA CTT TAT SD Met Glu Phe Lys Lys Leu Tyr a SIGNAL PEPTIDE_a a >	180 8
	GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT TTA ACA AGT GTC CAA GCA Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala> a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a	240 28
	ATA AAT GTT AGT CAA CCA TCT AAT AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys> b b b b b b b b b b b b b b b b b b b	300 48
	ATT GAT AAT AGT CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp> b b b b b MATURE PEPTIDE b b b b b b b c b c c b c c c c c c c	360
	GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA AAT TTA Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu>	420 88

CA CTT AGA er Leu Arg b b b containe Ser la 11e Ser la 11e Ser la 12e Ser la 13e Ser la	CA CTT AGA GCT AAT CCT GAA ACA ATT TAT GAT TTA AAT TCG ATT GGA ACA AGA SET Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg> b b b b b b MATURE PEPTIDE b b b b b b b b b b b b b b b b b b b	GA 480 rg> 108
13 C.	ACT GTG CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT AGA GCA ACT ATT TAC GTT Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val> b b b b b b MATURE PEPTIDE b b b b b b b b b b b c b c c c c c c	TT 720 al> 188
A G1 u A6 - b	AAA TTA GAC AAG CTT ATT TGG CAA ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT Lys Leu Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu> b b b b b b b b b b b b b b b b b b b	TT 780 eu> 208
	AAG AGT TTT GAA GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly> b b b b b b b mATURE PEPTIDE b b b b b b b c b c c c c c c c c c c	GT 840 1y> 228

JTA 7a]	TA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG CTA CAA eu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val Leu Gln> b b b b mATURE PEPTIDE b b b b b b c b c c	900 248
34.	TA AAT ACT GCT CTA CAG TAAGGTAGAGATTGAATTGA	960
	TTAATTTCAGTCCTTTAGAATTTTTATTTAGCTGATTTACTTGTTGAAGAGA	1020
. T.	AAAATCAAGTACCATACTTCTTCTCCTCCAAATACTTGTATGTCGATTCC	1080
	ACATAGCTAATTAGTTTTCTGGCTAATAGATTGTACATGAAATTGTT	1140
ZAZ	CTAGGGTAAAAGGTTTTTTTTTTATAAATTCATGACTAT	1190

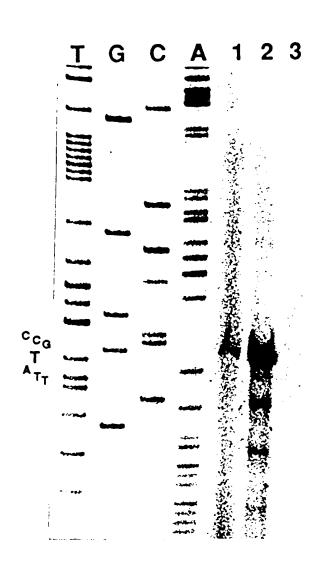


FIG. 5

SUCAMP	1	MEFKKLLYLTGSIAGITLFSPILTSVQANQINVSQP	-45
SAGCAMP	1	DQVTTPQVVNHVNSNNQAQQMA -22	-22
SUCAMP	ı	QKKEEIDNSLNQESAQLYALKEDVKGTEKEQSVNSAISAVENLKTSLRAN -95	-95
SAGCAMP	1	QKLDQDSIQLRNIKDNVQGTDYEKPVNEAITSVEKLKTSLRAN	-65
SUCAMP	1	PETIYDLNSIGTRVEAISDVIQAIVFSTQQLTNKVDQAHIDMGFAITKLL -145	-145
SAGCAMP	ı	SETVYDLNSIGSRVEALTDVIEAITFSTQHLANKVSQANIDMGFGITKLV -115	-115
SUCAMP	1	IRIADPFASNESIKGQVEAVKQVQATVLTYPDLQPTDRATIYVKSKLDKL -195	-195
SAGCAMP	1	IRILDPFASVDSIKAQVNDVKALEQKVLTYPDLKPTDRATIYTKSKLDKE	-165
SUCAMP	1	IWQTRITRDQKVLNVKSFEVYHQLNKAITHAVGVQLNPTVTVAQVDQEIK -245	-245
SAGCAMP	1	IWNTRFTRDKKVLNVKEFKVYNTLNKAITHAVGVQLNPNVTVQQVDQEIV -215	-215
SUCAMP	ı	VLQEALNTALQ -256	
SAGCAMP	l	: ::::: TLQAALQTALK -226	

12345678

+ + + CAMP reaction

F/G. 7

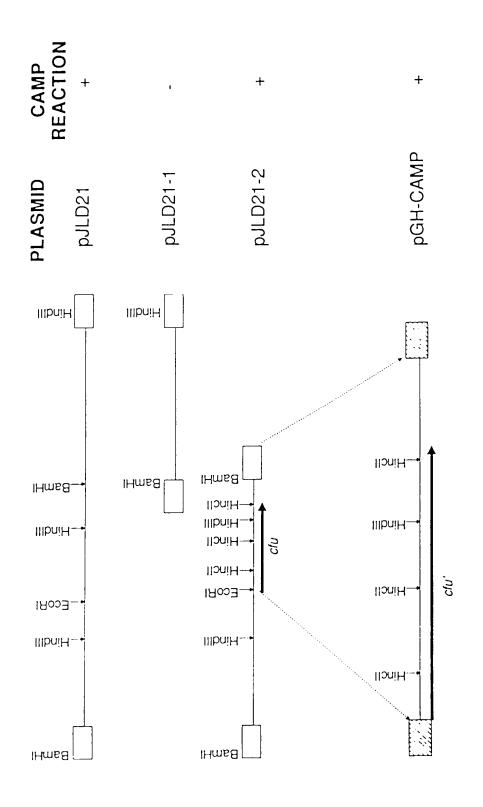


FIG. 8